

150

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HP02573 61' YGRQDLHLRI FDPSPEDIARADNI FTATERNRIDYSSAVRIDHAPDLPRPEVCFIGRSN
      . . . . . * * * * *
      MFFAQPVSFIMGAVRMDAMP PSDLPEVAFAGRSN
Cgpa 1"
HP02573 121' VGKSSLIKALFSLAPEVEVRVSKKPGHTKKMFFKVGVKHFTTVVDMPGYGF-----RAPED
      * * * * * . . . . . * * * * *
Cgpa 35" VGKSSLLINGL--VNQKYLARASNEPGRTRQINFFLLAEKVRLVDLPGYGFARVRSR SIADK
      * * * * * . . . . . * * * * *
HP02573 176' FVDMVETYLKERNLKR TFLIVDSVVG IQKTDNIAIEMCEE FALPYVIVLT KIDKSSKGH
      * * * * * . . . . . * * * * *
Cgpa 93" FQDLGRAYLRGRANLKR VYVLIDARHGLKKVDLEALDALDVAAVSYQIVLTKADKIKPAE
      * * * * * . . . . . * * * * *
HP02573 236' LLKQVLQIQKFVNMTQGC FFPQLFPVSAVTFSGIHL LRCFIASVTGSLD
      * * * * * . . . . . * * * * *
Cgpa 153" VDKVVAETQKAIKRAAA-FPRVLAT SKEKGLGMP ELRAEIVRLCIDE
      * * * * * . . . . . * * * * *

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HP02612   61'  KVP LAGGRK PRLHRRHRVYKLVEDTKHRPKENLELILTQSVENVGVRGDLVSVKSLGR
          ..***...* * * * *
          MKLILTADVDHLGSGVDTVEVKDGYGR

RL9_MYCLE 1"

HP02612   121' NRIIPQGLAVYASPENKKLFEEEEKLLRQEGKLEKIQTKGAGEALGVVVAPHITIKLPAPETIT
          * ***.***. .... . * * * * . . . . . * * * * *

RL9_MYCLE 28" NFLIPHGLAIVASRGAQRQADEIRRAR-ETKAMRDREHANEIKVAIEALGSVSLPMKTVA

HP02612   181' RWGEYWCEVTVNGLDITVRVPMVSVNFEKPCTKRKYWLAQQAAKAMAPTSPQI
          * . . *.***. .... . * * * * . . . . .

RL9_MYCLE 87" DSGKLFSGTVTAGDVVAAIKKAGGNLDKRIVRLPKTHIKAVGTHPVSUHLHPEVDVVLL
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61' KAKGQSQTRVNINAALVEDIINLEEVNEEMKSVIEALKDNFNKTLNIRTSFGSLDKIA
    ** ..... * ..... *** ..... * ..... * .....
RRF_BRUME 1" MSDAFDINDLKRRMEGAVNALKHDLGGLRTGTRASASLLEPIT

121' VVTADGKLALNQISQISMKSPQLILVNMAFFPECTAAAI-KAIRESGMNLNPEVEGTILR
    . . . . . ** ..... * ..... . . . . . *** ..... * ..... * .....
RRF_BRUME 43" IEYGSTMPINQVANISV--PESRMLSVSVWDKSMVGAVERAIRDSGLGLNPITDGMTILR

180' VPIPQVTRHREMLVKLAKQNTNKAKDSLKVRRTNSMNKLLK-KSKDT-VSEDTIIRLIEKQ
    *** ..... ** ..... * ..... * ..... * ..... * ..... * .....
RRF_BRUME 101" IRLPELNEQRRKELVKIAHQYAEQGRIAAHVRRDGMQDLKKLEKDSVISQDESRLVSEK

238' ISQMADDTVAELDRHLAVKTKELIG
    . . . . . ** ..... * ..... * .....
RRF_BRUME 161" VQKLTDYTTIAEMDKIVAVKEGEIMQV

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Fig. 4

HP10120	1'	MQRVSGLLSWTLRVLWLSGLSEPGAARQPRIMEE-KALEVYDLIRTIRDPKPNTLEEL
CEF45G2		*... *... *... *... *... *
HP10120	1"	MGQERLDNANPTLFDKPRHRPVTGTERDESVEPDIDSWEIFDLIRDINDPEHPYTLLEQL
CEF45G2		*... *... *... *... *... *
HP10120	60'	EVVSESCVEVQEIINEEYLVIIIRFTPTVPHCSLATLIVGNLHF
CEF45G2		*... *... *... *... *... *
HP10120	61"	NVVQEELIKV-FIDEEETFVKVNFPTTIPHCSMATLIGLAIRVKLLRLSLHPKVVSISIT
CEF45G2		*... *... *... *... *... *

Fig. 5

HP10421 1' MAAAGLALLCRRVSSALKSSRLITPQVPACTGFFLSLLPKSTPNVTSEHQYRLLHTLS
 B0261.4 1" MGEAIVRWSALAAHLLFFGSKVFSKIFYFLMFFKSTMWRSLPSLVS-SAVRSQNAVNT
 HP10421 61' R--KGLEEFFDDPKNWG---QEKVKSAAWTCQQLRNKSNEDLHKLWYVLLKERNMLLT
 B0261.4 58" RFSSTMKQFFDDEANFGKAELRPKHPGRSWTAELRLKSNSDLHKLWYVCLKERNMLIT
 HP10421 115' LEQEAKRQRLPMPSPERLDKVVDSDMDALDKVVQEREDALRLLTGTGQERARPGAWRRDIFG
 B0261.4 118" MKKAHTSRARNMPNPERLDRVHETMDRIESVVHERNDVFRLETG-ESAAPRKRTITSA
 HP10421 175' RIIWHK-FKQWVIPWHL-NKRYNRKRFEPALPYVDHFLRLERE---KRARIKARKENLERK
 B0261.4 177" GFTYQKQATEHFAPPQLGQKEYETPYLDDDDAYVMQKIQEKEFFMKNRDRLLDDEKRRRAART
 HP10421 230' KAKILLKKFPFLAEAKSSLV
 B0261.4 237" EDMDRFKRGAPRVFNR

Fig. 6

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HP10582      1'      MDSNHQSNYKLSKTEKKFLRKQIKAKHTLLRHE-GIETVSYATQSLVVANGGLGN
                * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 361"  RELSYFNEEKAKRIGERFEGGKLAKKVHKISIEQLKRHDPDVQISTEPTKYLLVSNSSILC

HP10582      55'      GVS RNQLLPV-LEKCGLV DALLMPPNKPYPFARYRTTEESKRAYVTLNGKEVVDLGLQKI
                *** . . . * . * . . . * . * . . . * . * . . . * . * . . . * .
YKY5_CAEEL 421"  GVSLEEELEEIFLPLDELAEFIVYPNKRYSFVQCSSIEKSIQVRTELHGLIPPSLKNSHQ

HP10582      114'     TLYLNFVEKVQWKELRPQALPGLMVVEEIISSSEEEKMLLESVDWTEDTDNQNSQKSLKH
                . . . . . * . * . . . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 481"  PFAISYVENLPEATKCEDFRPANLKIIEEYVSSDLEKELVDLV-----TNHPSVQSLKH

HP10582      174'     RRVKHFGYEFHYENNVNVDKDKPLSGGLPDICESFLEKWLKGYIKHKPDQMTINQYEPGQ
                * * * * . * . * . . . . * . * . . . . * . * . . . * . * . * . * .
YKY5_CAEEL 535"  RAVVHFHGVFDYSTNSASEWKE-ADPIPPVINSLIDLRLISDKYITERPDDQVTANVYESGH

HP10582      234'     GIPAHIDTHSAFEDEIVSLSLGSEIVMDFKH--PDGIAVPVMLPRRSLLVMTGESRYLWT
                *** . * * * * * . * * * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 594"  GIPSHYDTHSAFDDPIVSI SLSDVVMEFKDGANSARIAPVLLKARSLCLIQGESRYRWK

HP10582      292'     HGITCRKFDTVQASESLKSGIITSDVGDLTLSKRGLRTSFTFRKVRQTPCNCYSYPLVCD
                *** . * * . * . * . * . * . * . * . * . * . * . * . * . * . * .
YKY5_CAEEL 654"  HGIVNRKYD-----V-----DPRTNRVVPVRQTRVSLTLRKIRKPKCECEWKEFCDW

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Fi 8. 6-1

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HP10582 352' QRKETPPSFPESDKEASRLQEQYVHQVYEEIAGHFSSSTRHTPWPPIVVEFLKALPSGSIVA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
YKY5_CAEEL 700" DRKGE-MSVPSNEDLALKLENSYVSDVYENIASHFDETRHSSWKAVKQFINEIPRGSVMY
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
HP10582 412' DIGCGNGKYLGINKELYMERRVAALQEIVRLLRPGGKALIYVWAMEQYNKQSKYLRGN
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
YKY5_CAEEL 759" DVGCGNGKYL-IPKDGLLKIGCDMCMGLCDIARKKDCHVARCDALALPF-----RYESAD
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
HP10582 472' RNSQKKEEMNSDTSVQSRSLVEQMRDMGSRDSASSVPRINDSQEGGCNSRQVSNKLPVH
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
YKY5_CAEEL 813" AAISIAVLHHIATFERRKRRLIEELLRVVKPGSKICVT-VWSMDQSQSEYAKMRGNKDDV-
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
HP10582 532' VNRTSFYSQDVLVPWHLKGNPDKG-KPVEFPFGPIGSQDPSPVFHRYVHVFREGELEGACR
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
YKY5_CAEEL 871" AAPAVSSEETQTNRLLKVHDGKDFEQQDVLVPWTIDQKGETFLRYVHVFREGEAEKLE
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
HP10582 591' TVSDVRILQSYDQGNWCVILQKA
      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
YKY5_CAEEL 931" SVQGCKLLISVEKEQGNY-IIIIAKKI

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Fig. 8

HP10160	1'	MASRGKTETSKLKQNL	EEQLDRMQQLQDL	EECREELDTDEYEETKKETLEQLSEFNDSL
ZK1248	1"	MGVDDLLIKNAQKTIDRLIRQLAEIEQ	EENNLEDEYRELREDTVNQLEYGKIV	
HP10160	61'	KKIMSGNMTLVDEL	SGMQLAIQAISQA	FKTPEVIRLFAKKQPGQLRTRLAEMDRDLMVG
ZK1248	56"	ERLQGGDVSLIDDLTATKIAIRTAISKA	FKTPEIMALFAGKHTGLLREKLM	TETNYRSQ
HP10160	121'	KLERDLYTQQKVEILTALRKLG	EKLTADEAFLSANAGAILSQ	FKEKVSVDLGSGDKILAL
ZK1248	116"	KMPKQGYLERKFEILMALRRLEETL	TEDEKFLSDRLET--PEFQLIEANANRL	FSGNVT
HP10160	181'	ASFEVEKTKK		
ZK1248	174"	SPVFRVQIMASPKPKKVR	LDKTEENVSPWKAWWHTEKKRKFYTNDK	TKESLWDHPNTR

HP10173	1'	1' MKLLTTHNLLSSHVRGVGSRGFPLRLQATEVRICPVFENPNFVARMI PKVWSAFLEAADN ***...***. *...* *...* *...* *...* *...*
C04H5	1"	1" MKLFVHNFMSRFLKNVTVGYPNLNVVKQFVEKDIFFDRDNTFIVMLDRIQYEALIVAAAA
HP10173	61'	61' LRLIQ-VPKGPVEGYEE-NEEFRTMHHLLEVEVIEGTLCQPESGRMFPI SRGIPNMLL * . . . * *...* *...* *...* *...* *...*
C04H5	61"	61" VNQSDRIPREKPEKWDLTDEQLRVFHHLLMNIDVIDGELICPETKTVPPI RDGIPNMLK
HP10173	119'	119' SEEETES .. *
C04H5	121"	121" VDAEK

Fig. 10-1

HP02644 300' DDTVIESEALPSDIAAEARAKTGTGTVSDQALLFGDDDDAGEGPSSLIREKFPVKQNEENEENE
CELLF55F8 263' -----
HP02644 360' NLDKEQVGNLQKELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVARFTGIKTA
CELLF55F8 323' -----
HP02644 420' ILVGMSTQKQORML-NRRPEIVVATPGRLWELIKEKHY--HLRNLRLQLRCLVVDEADRM
CELLF55F8 383' SIVGGLAQVKQERIIISQORPDIIVATPGRLWAMMQEAEYGEFLAEWKDLKCLVVDETDRM
HP02644 477' VEKGHFAELSQLEMLNDSQYNPKRQTLVFSATLTLVHQAPARILHKKCHTKQMDRTAKLD
CELLF55F8 443' VEEGYFAELTHILNKIHEESEKELQTLVFSATLTFAKAQDVAEEFKCKAKELSSQQKIQ
HP02644 537' LLMOQKIGMR-GKPKVIDLTRNEATVETLTETKIH CET-DEKDFYLYCYFLAQYPGRSILVFA
CELLF55F8 503' RLILKLTGLRENKHKVIDLTROMGTAGCLVEARINCGNLLLEKDTSLVYLLTRYPGRTIVFV

Fig. 10-2

[illegible]

Fig. 11

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HP03233      1' MAAPGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQEKRAAETHFGFETVVS
              ...*.* * * * * .. * . . . . . *****
SPUBM        1" MSRLRAPVAKFLADGLKGIRSTALAGURLSN-CRYTSTSSKDDTDTSSHMTTHFGFKDVP

HP03233      61' EEEKGGKVYQVFESVAKKYDVMDNMMSLGIHRVWKDLLWKMHPLPGT---QLLDVAGGT
              ***.* **..***** *** *******.....*.* .....*****
SPUBM        58" EDEKEHLVKNVFSSVAKKYDEMNDAMSLSLGIHRLWKNI FVSR LNPNGNSTVPMKIL DVAGGT

HP03233      118' GDIAFRFLNYYQSQHQRKKQLRAQQNL SWEETAKEYQNEEDSLGGSRVVVCDINKEML
              *****... ..*.* .....
SPUBM        118" GDIAFRILNHATNHNGDRNRVIV-----ADINPDMML

HP03233      178' KVG-KQKALAQQYRAG-LAWVLGDAEEL-PFDDDKFDIYTIAFGIRNVTHIDQALQEahr
              **... ..*.* ....**.* ..*....***** **** .....***
SPUBM        150" SVGLRRSKKTPYYDSGRVEFIEQNAEILDKIPDNSIDMYTIAFGIRNCTHIPKVLEQAyR

HP03233      235' VLKPGGRFLCLEFSQVNPNLISRLYDLYSFQVIPVLGEVIAGDWKSYQYLVESIRRFPSQ
              ***** * ****** . . . ** ******.***.***** .....*****
SPUBM        210" VLKPGGVFSCLEFSKVYPAPLAELYRQYSFKILPLLGTIIAGDSQSYEYLVESI ERFPDA

HP03233      295' EEFKDMIEDAGF---HKVTYESLTSGIVA IHSGFKL
              ..* ..***** ..*.*.* ..*.*.*.*..*.*

SPUBM        270" KTFakmiedagFTLAGETGYETLSFGIAAIHTGIKL

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Fig. 12

1' M0KSC0E0EN0GK0P0Q0M0P0K0A0E0D0R0P0L0E0D0V0P0Q0A0E0G0N0P0Q0P0S0E0E0G0V0Q0A0E0G0N0P0R0G0G0P0Q0P0G0Q0
 1" MKSCQKMEGKPN---ESEPKEHEEPKPEEKPEEEKLEEEAKAKGTFRERLIQSLQE
 61' FKEDTPVRHLDP0E0M0I0R0G0V0D0E0L0E0R0L0R0E0I0R0R0V0R0N0K0F0V0M0H0W0K0R0H0S0R0P0Y0P0V0C0F0R0P
 56" FKEDIHNRHLSNEDMF0E0V0D0E0I0---D0E0I0R0R0V0R0N0K0L0I0V0M0R0W0K0V0N0R0H0P0Y0P0L0M

Fi. 13

Fig. 14

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HP10543 1' MAATEPILAAATGSPAAVPPEKLEGAGSSSAPERNCVGSLLPEASPPAPEPSPNAAVPEA
      .. ... * * * * *
LEAP1 1" MAAQPSQDPQSPAAPPEQQEGAGDCA

HP10543 61' IPTPRAAASAALELPLGPAPVSVAPQAEAEARSTPGPAGSRLGPETFRQFRQFRYQDAA
      ** ... ** *** ** ... ** * ** * * * * *
LEAP1 28" APSDGS SSPAPELPGAPAAINTAPYADAVLR---PGASRPGPETFRQFRQFRYQDAA

HP10543 121' GPPEAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQLLAILPEAARARRRRRTDVRITG
      * * * * *
LEAP1 84" GPPEAFRQLRELSRQWLRPDIRTKEQIVEMLVQEQLQAILPEAARARRLLRRRADVRITG

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Fig. 15

HP03090 1' MAARRALHFVKVGNRFQTARFVRLVGLMKVLRHEEFEEGCKAACNGPYDGKWSKTMVGF
 CEHYPO 1" M'ARALHYVFKVANRAKTIDFFTNVLNKMVLRHEEFEEGCKEATCNGPYNGRWSKTMIGY
 HP03090 61' GPEDDHFVAELTYNYGVGDYKLGNDFMGITLASSQAVSNARKLEWPLTEVAEGVFETEAP
 CEHYPO 60" GSEDEHFVLEITYNYPIHKVELGNDYRAIVIDSDQLFEKVEKIN--HRKSGCGRLAVKDP
 HP03090 121' GGYKFYLNQNRSLPQSDPVLKVTLAVSDLQKSLNYWCNLLGMKIYEKDEEKQALLGYADN
 CEHYPO 118" DGHEF--KIGKADQSPKVLRVQNVNVDLEKSKKYWNETLGMPIVEEKSSRIR--MSYGDG
 HP03090 181' QCKLELQGVKGGVDHAAAFGRIFAFSCPQKELPDLEDLMKRENQKILTPLVSLDTPGKATV
 CEHYPO 174" QCELEIVKSQDKIDRKTFGRIFAFSYPEDKLESQDKIKSANGTIINELTTLETTPGKADV
 HP03090 241' QVVILADPDGHEICFVGDEAFRELSKMDPEGSKLLDDAMAADKSDEWFAKHNKPKASG
 CEHYPO 234" QVVILADPDEHEICFVGDEGFRALSKIDDKAESLKEQIKKDDSEKWI

Fig. 16

HP03145 1' MLGSRAGFARGLRALAWLPGWGRGRSFALARAAGAPHGGDLQPPACPEPRGRQLSLSA
SCCOQ2 1" MIIKPIASPARYFLRTPSWSAVAIFQAVKIKPLQLRRTNSSNSVTPNLISPSK
HP03145 61' AAVVDSAPRPLQPYLRIMRLDKPIGTWLLYLPCTWSIGLAA---EPGCFPDWYMLSLFGT
SCCOQ2 53" KSWKDLFSKRWQYVAEISRAGSPTGTLYLLYSPCTWSILMAAYAYDSSLVNVTKMLALEGV
HP03145 118' GAILMRGAGCTINDMWDQDYDKKVTRTANRPIAAGDISTFQSFVLGGQLTLALGVLLCL
SCCOQ2 113" GSFLMRGAGCVINDLWDRELDKAKVERSKSRPLASGKLSVRQAISSLVQLTASLGILLQL
HP03145 178' NYYSIALGAGSLLLVITYPLMKRISYWPQALGLTFNWGALLGWSA IKG-SC-DPSVCLP
SCCOQ2 173" NPYTIKLGVASLVPCITYPAMKRITYYPQVVLGLTFGYGAVMGWPALAGEACMNWSVVAP
HP03145 236' LYFSGVMWTLIYDTIYAHQDKRDDVLLIGLKSTALRFGENTKFWLSGFSVAMLGALSLVGV
SCCOQ2 233" LYLSTISWIVLYDTIYAHQDKRDDVKANIYSTALRFGDNTKFWLCCGLAALQIATLATAGI
HP03145 296' NSGQ'TAPYYA-ALGAVGAHLTHQIYTLDIHRPEDCWNKFISNRTGLIVFLGIVLGNLWK
SCCOQ2 293" MNGQGPVFTYTLGVAGAAVRLSSMIYKVDLDDPKDCFRWFKRNSNTGYLVAAAIALDWLAK
HP03145 355' EKRTDKTKKGIENKIEN
SCCOQ2 353" SFIYDS

Fig. 17

[illegible]

Fig. 20

HP10162	1'	MEPQEERETQVAAWLKKIFGDHPPIQYEVNPRTEILHHLSENRVRDRDVYLVIEDLKQ
RNUNK	1"	MAALEEKASQVAEWLKKIFGDHPPIQYEMNARTTEILYHLSERNVRDRDVNLVIEDLRP
HP10162	61'	KASEYESEAKYLQDLLMESVNFSPANLSSTGSRYLNALVDSVALETKDTSLSAFIPAVN
RNUNK	61"	KASEYESEAKRLIEDFLMESVNFSPANLSNTGSRFLNALVDSIALEIKDTSLSAFIPAVN
HP10162	121'	DLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDVKKAEHLSTERAKVDNRRQ
RNUNK	121"	DLTSDLFRTKSKSEEIKLEIGKLEKNLTATIVLEKCLREDLKKADVHLSAERAKAEGRLQ
HP10162	181'	NMDFLKAKSEEFRRFGIKAAEEQLSARGMDASLSHQSLVALSEKLARLKQQTIPLKKKLES
RNUNK	181"	NMDFLKAKAAEFRRFGIRAAEEQLSSRGMDASLSHRSLVALSDKLSELKQQTIPLKKKLES
HP10162	241'	YLDLMPNPSLAQVKIEEAKRELDLSIEAELTRRVDMMEL
RNUNK	241"	YLDLMPNPSLAQVKIEEAKRELDLSIEAELTKKVDMMEL

HP10334 1' MSGLRVYSTSVTGSREIKSQSQSEVTRILDGKRIYQLVDISQDNALRDEM R---ALAGNP
 HSSH3 1" MVIRVYIASSSGSTAIAKKKQDVLGFLEANKIGFEEKDIAANEENRKWMRENVVPENS RP
 HP10334 58' KAT'--PPQIVNGDQYCGDYELFVEAVEQNTLQEFFLKLA
 HSSH3 60" ATGYPLPPQIFNESQYRGDYDAFFEAARENNAVYAFGLGLTAPPGSKEAEVQAKQQA

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Fig. 22

HP10532	1'	MAGSEELGLREDTLRVLAFLRRGEAAGSPVPTPPRSPAQEEPTDFLSRLRRCLPCSLGR
HSBBK	1"	MAGSEELGLREDTLRVLAFLRRGEAAGSPVPTPP-SPAQEEPTDFLSRLRRCLPCSLGR
HP10532	61'	GAAPSESPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGPST
HSBBK	60"	GAAPSESPRCSLPIRPCYGLEPGPATPDFYALVAQRLEQLVQEQLKSPSPPELQGPST
HP10532	121'	EKEAILRRLVALLLEEEAEVINQK-----EGILAV
HSBBK	120"	EKEAILRRLVALLLEEEAEVINQKLASDPALRSKLVRLSSDSFARLVELFCSRDDSSRPSR
HP10532	181'	-----EGILAV
HSBBK	180"	ACPGPPPPSPEPLARLALAMELSRRVAGLGGLAGLSVEHVHSFTTPWIQAHHGWEGILAV
HP10532	241'	SPVDLNLPLD
HSBBK	240"	SPVDLNLPLD

Fig. 24

HP10562 61' QESEPEDFLKLFIDPNEVCSEASPGSDSGISEDPCHPDSPAPRATSSPMLYEVVYEAG
LZIP 1" MELELDAGDQDILLAFLEESGDLGTAPDEAVRAPLDWALPLSEVPSPDWEVDDDL
HP10562 121' ALERMQGETGPNVGLISIQDQWSPAFMVPDSCMVSELPFDAHAILPRAGTVAPVPCIT
LZIP 54" LCSSLSPPASLNILSSSNPCLVHHDHTYSLPRETVSMDLESESCRKEGTQMTPOQHMEELA
HP10562 181' LLPQCFTLTDEEKRLGQGVSLPSHLPLTKAEERVLKKVRRKIRNKQSAQDSRRRKKKE
LZIP 114" EQETARLVLTDEEKSLLLEKEGLILPETPLTKTEEQILKRVRRKIRNKRSQAQESRRKKKV
HP10562 241' YIDGLESRVAAACSAQNQELQKKVQELERHNI SLVAQLRQLQTLIAQTSNKAQTSTCVLI
LZIP 174" YVGGLESRVULKYTAQNMELOQNVQVLLLEEQNLSLLDQLRKLQAMVIEISNKTSSSSTCILV
HP10562 301' LLFSLALIILPSFSPFQSR----PEAGSEDYQPHGVTSRN--ILTHKDV TENLETQVVES
LZIP 234" LLVSFCLLLVPAMYSSDTRGSLPAEHGVL SRQLRALPSEDPPYQLELPALQSEVPKDSHTQ
HP10562 355' RLREPPGAKDANGSTRTLLEKMGKPRPSGRIRSVLHADEM
LZIP 294" WLDGSDCVLQAPGNTSCLLHYMPQAPSAEPPLWFFDLFSEPLCRGPILPLQANLTRKG

HP10456	1'	MSNMEKHLFNLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAEN *****
CEBC-2	1"	MGAGESMALEKHLFDLKFAAKQLEKNAQCEKDEKVEKDKLTAAIKKGNKEVAQVHAEN *****
HP10456	55'	AIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVKSMDATLTKTMNLEKISAL *****
CEBC-2	61"	AIRKKEAVNYIKMAARIDAVAARVQTAATQKRVTA SMSGVVKAMESAMKSMNLEKVKQQL *****
HP10456	115'	MDKFEHQFETLDVQTOQMEDTMSSTTLTTPQNQVDMLLQEMADEAGLDLNMELPQGQTG *****
CEBC-2	121"	MDRFERDFEIDLDTTKTMEKTMDDGTTVLNAKPSQVDALIAEADKAGIELNQELPSNVPT *****
HP10456	175'	SVGTSV-ASAEQDELSQRLARLRDQV *****
CEBC-2	181"	ALPTGTQAVSEDKDLTERLAALRNM *****

Fig. 26

HP10498	1'	MATPSLRGLARFGNPRKPVLPKPKPLILANRV-GERRREKGEATCITEMSVMA
CEC24	1"	MMFSSPLLKEKALARGKSIYPKVAVFSEILPLASKNRVQAGQKPRAASSSCTQELQALFG
HP10498	55'	CWKQNEFRDDACRKEIQGFIDCAAR-AQEARKMR--SIQETLGESGSLLPNKNLKLQRF
CEC24	61"	CLKKWEFDDVPCSKQHTLYMDCVHKGAEEAAAYRDATRKGTLGESGAGGKQSMTSAQFNK
HP10498	112'	PNKP YLS
CEC24	121"	IQKLFPQPDLGKQPYRQMKRLPTQDYADDTFHRKHWSGKRS

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Fig. 27

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HP10505   1' MAKHLKFIA RTVMVQEGNVESAYRTLNRI L TMDGLIEDIKHRRYYEKP CRRRQRRESYERC
          ***** **..*****.***
CEF29     1" MVQNNDVDGAFGLLNRLIMDSEGMLKIIRRTQFYQKPYMQRKLTLSMEAS

HP10505   61' RRIYNMEMARKINFLMRKNRADPWQC
          *.**.*.*.*.*.*.*.*.*
CEF29     49" TAIFNEDMNRKMKFLVRKNRPDKHPGGQVTS

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HP10515 1' MFLTAL-LWRGRIPGRQWIGKHRRPRFVSLRAKQNMIRRLRLIEAENHYWLSPYMTREQE
          * * * . * . . * * * . * * * * * * * * * * * * * * * * * *
DM63B   1" MHLTILNLFKKTVPGHIFRGKRRLLVKPVSQRAMDTLTREYERQEQVMLLLRHPYLTMEQS
          * * * . * . . * * * . * * * * * * * * * * * * * * * * * *
HP10515 60' RGHA-AVRRREAFE--IKAAATSKFPPHFRFIADQLDHLNVTKKWS
          *** . . . . . * * . . . . * * * * * * * * * * * * *
DM63B   61" FGHAKELQKREKLVARWTDEQTLRKQKPHVTTIEERLNQLKIKEAWD
          * * * . . . . . * * * * * * * * * * * * * * * * * *

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Fig. 29

HP01124	1'	MGTEKESPEPDCQKQFQAAVSVIQNLPKNGSYRPSYEMLRFYSYKQATMGPCLVPRPG
HSACBP	1'	MSQAEEFEKAAEEVRHL-----KTKPSDEEMLFIYGHYKQATVGDINTERPG
HP01124	60'	FWDPIGRYKWDawnSLGKMSREEAMSAYITEMKLVAQKVIDTVPLGEVAEDMFGYFEPLY
HSACBP	47"	MLDFTGKAKWDawnELKGTskEDAMKAYINKVEELKKYGI

Fig. 30

HP02241	1'	MRLSALLALASKVTLP	PHYRYGMSPPG	SVADKRNPPWIRRPVVVEPI	SDWDWYLF	CGD
		***	***	***	***	***
XLRPL24	1"	MRLTLLLEMAAKLKLPHDYRFGMSRPS	STLAKRRNPPGKR	RSKVFEVPSKEEWQYFRGD		
		***	***	***	***	***
HP02241	61'	TVEILEGKDAGKQGVVQVIRQ	RNVVVGG	LNTHYRYIGKTM	DYRGTMIPSEAP	LLHRQV
		***	***	***	***	***
XLRPL24	61"	TVEVLHGKDAGKQGVVQVVRARNVVVD	GLNTHFRYVGR	TDEYRGTYVASEAP	LLLNQV	
		***	***	***	***	***
HP02241	121'	KLVDPMDRKPT	IEWRFT	EAGERVSVSTRSGRIIPKPEFP	PRADGIVPETWIDGPKDTSVE	
		***	***	***	***	***
XLRPL24	121"	SLIDPTDRKPT	IEWRYTEGERVRS	ARGRIIPKPV	LQRRDGIIP	EQWKDGP
		***	***	***	***	***
HP02241	181'	DALERTYVP	CLKTLQEEVMEAMG	IKETRKYKKV	VWY	
		***	***	***	***	***
XLRPL24	181"	DALERTYVP	SLKTFQEEIMEKTGIAENR	STGNPTGTNP	GRAVRSNHN	SHCSC
		***	***	***	***	***

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HP10101 1' MKAVKSERERGSRRHRDGDVVLPAQVVVKQERLSPEVAPPAHRRPDHSGGSPSPPTSEF
HP10101 60' ARSGHRGNRARGVSNPSPKKKNKASGRRSKSPRSKRNRSPHHSTVKVKQEREDHPRRGRE
CEC32E8 1' MGRDSPDRRRHRDRSPERRRRSRSRDRQTRRD-T
HP10101 121' DRQHREPSEQEHRRRARNSDRRHRGHSHQRRTSNERPGSGQGQGRDRDTQNLQAQEEERE
CEC32E8 36" RRDDSPKIKREVKEEQFSDNDSPPRRRRDRGGRRDRDRDRNRDDR-RDHRDDRGDRDRDR
HP10101 181' FYNARRREHRQRNDVGGGSESQELVPRPGNNKEKEVPAKEKPSFELSGALLIEDTNTFR
CEC32E8 95" NF--RRDPVREDGKQYGLEKKEENWGKPEEPAKEK-----EKVNLGTSGALTEDTNTFR
HP10101 241' GVVIKYSEPPEARIPKKRWRLYPFKNDEVLPVMIYIHRQSAVLLGRHRRRIADIPIDHPSCS
CEC32E8 148" GVVIKYNPEPAKKPNARWRLYPFKGEEGLQVLIYHRQSAVLLIGRDHKIADIPVDHPSCS
HP10101 301' KQHAVFQYRLVEYTRADGTVRRVKPYIIDLGSNGTFLNNKRIEQRYRYELKEKDVLKF
CEC32E8 208" KQHAVLQFRSMFPFTRDDGTKARRIMPYIIDLGSNGTFLNEKKIEPQRYIELQEKDMLKF
HP10101 361' GFSSREYVLLHESDTSFIDRKDDDEDEEEEEEVSDS
CEC32E8 268" GFSTREYVVMKEREITEEELAEGEDVKKKEESD

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HP10101 361" GFSSREYVLLHESSTSEIDRKDDDEFEFEFEVSDS
 .** ** ***.
 CEC32E8 268" GFSTREYVVMKEREITEEEELAEGEDVKKKEESD

Fig. 32

HP10370 1' MEYDEKLARFRQAHLNPFNKQSGPRQHEQQPGFEVDPVTPKALPELPPGEPEF
 DMC115 1" MSSWKDSLTSGTVAQLINESASNLHSSSTLGSTVGLGGSGTSGGSEAGGSEESGPQ
 HP10370 55' RCPERVMDLGLBEDHFRSPVGLFIASDVQQLRQAIEECKQVILELPEQSEKQKDAVVRLL
 DMC115 61" GAERYALPFPASIVREQWRLITFSDANIQDLQAAIAHCNDLVLLSEELSEERRWLVRHLV
 HP10370 115' HLRKLQELKDPNE-----DEPNIRVLEHNE-----YKEKSKSVKQTC DK
 DMC115 121" DLRYGLQELEEAQEQHSLSSDMVMNAIRAVVGHIFVPIPHIHGKRRLQAAAKRNYCDH
 HP10370 156' CNTTIWGLIQTWYTCGYYRCHSKCINLISKPCVSSKVSHQAEYELNICPETGLDSQDY
 DMC115 181" CFTTIWVVQNSVVCSDCGFLVHQKCIDGVKRVCAINVLVSEHQHPISEICPEIGLASQGY
 HP10370 216' RCAECRAPISLRGVSEARQCQDYTGQYYCSHCINWDLAVIPARVVHWNWDEFPRKVSRC SM
 DMC115 241" KCAECGTMLNIXNTWIEPRLCDYSGLYCPCRCNWNDSNFIPARIHWNWDFHPRRVSR TAL
 HP10370 276' RYLAIMVSRPVLRIREINPLILFYSVVEELVETIRKLQDILLMKPYFITCREAMKARLL-LQ
 DMC115 301" QEIRLFLNKPRLIRLEEDNPKLFVFEKLCVAVKKLRQNLVIMRHYLAACKIASSELKLVDDQ
 HP10370 335' LQDRQHFEVDEMYSVQDLLDVHAGRLGCSLTETHTLFAKHKLDCCERCQAKGFVCELCH
 DMC115 361" LGVRRHLAQSNFEFYBLSDLQSVEGALJEFLOGVFAFNHIR-SCPMCLAQAYICEICS
 HP10370 395' EGDVLFPPFDSHT"SVACDCSAVFHRDCYTDNSTTCPCKCARLSLRKQSLFQEPGPDVEA
 DMC115 420" NNEVIFPDDGCIKCDQCNSIFHRVCLTRKNMICPKCIRIQERRRLQDRMKSTEDDDDDDD

Fig. 33

HP10427 1' MAGPAAFRRLGALSGAAALGFASYGAH---GAQFPDAYGKELFDKANKHHFLHSLALLG
 ... ***** ** .. ** .. *****.
 CEY106G 1" MSPIIRLAGLSGAVAISLGAYGSHVLRDNP SIDERRRTAFDTASRYHLIHSALALA

HP10427 58' VPHCRKPLWAGLLLASGTTLECTSYYQALSGDPSIQTLAPAGGTLILLGLWALAL
 * * * * * .. ***** * .. * * * * *
 CEY106G 57" SPAARFPLVTAGLFTAGITLFCGPCYHYSISGVETTRKYTPIGGVTHIIAWLSFIL

Fig. 34

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1' MAGTGLLALRTLPGPSWVRGSGPSVLRLQDAAVVRPFGFLSTAEETLSRELEPELRRRRR
      . . . . . * * * * * * * * * * * *
DMCG141 1" MRIITDFISEPEEQQLHHEEIEPYMSRLR

61' YEYDHWDDAIHGFRETEKSRSWSEASRAILQRVQAAAFGGQTLSSVHVHLDLEARGYIKP
      * * * * * . . . . . * * * * * * * * * * *
DMCG141 29" YEFDHWDDAIHGFRETERKKWFKNREILERVQVAF--DGAVMPYVHILD LAPDGVIKP

121' HVDSIKFCGATIAGLSLLSPSVMRLVHT-----QEPG
      * * * * * . . . . . * * * * * * * * * * *
DMCG141 87" HVDSTRYCGNTISGISLLSDSVMRLVRTDEQRXQQSSGTATDPNSQGSEPDAA YRHQPE
      . . . . .

153' EWL-----ELLEPGSLYLIRGSARYDFSHEILRDEESFFGERRIPRGRRIISVICRSLP
      . * . . . * * * * * * * * * * * * * * * * *
DMCG141 147" ASLKNNFYADILLPRRSLYIMSHRTARYKFTHEILAKEHSQFQALVPRTRRIISICRNEP

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Fig. 35

HP10580 1' MKKFFQEFKADIKFK
DMCG546 61" TLLKVLIVLLGTCVLGYSWSIYGVKVTETKVRPSTLKEIEELKLSKAEAAFKLNLGTGS
HP10580 16' SAGPGQKLKESVGEKAHKEPNQ--PAPRPPRQGPTEAQMAAAALARLEKQKQSRWGP
DMCG546 121" GMGTGHLNLPKQETPSSSRQKYAYVPPKRNEISNEARAAAALARIDKRTSREFN-
HP10580 74' TSQDTIRNQVRKELQAEATVSGSP-EAPGTNVVSEPREEGSA-HLAVPGVYFTCPL-TGA
DMCG546 180" TSLSAVKAQAKRELEAEERRQREEAMGTPSTSTSTASGGDTRNLACEGVFFRCPLISEE
HP10580 131' TLRKQDQDACEIKAEAILLHFSTDPVAASIMKIYTFNKDQDRVKLGVDTIKYLNDNIHLHPE
DMCG546 240" ILPKSVWKVRIKEFLYQQLEADRGLTACLIHNCN-VKEKADECIATLIRYLENLIKNPE
HP10580 191' EEKYRKIKLQNKVFQERINCLGTHEFFEAIGFQKVLLPAQDQEDPEEFYVLSSETTLAQP
DMCG546 299" EEKFKIRMSNKIFSEKVRVVEGALDVLQAAGFNEV-----QIDGEPFLLTWKEQTEKD

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Fig. 35-1

HP10580 251' QSLERHKEQLLAAEPVRAKLDQRORRVFQPSPLASQFELPGDFFNLTAEIKREQLRSEA
 * * * * *
 * * * * *
 DMC546 353" LDLPTLVEALKSSEIIPLELDRNIKVLLPSQ-ACRVALPDEFYRLSPEEIKKEQQLRSEA
 * * * * *
 * * * * *
 HP10580 311' VERLSVLRTKAMREKEEQRLRKYNVTLLRVRLPDGCLLQGTFFYARERLGAVYGVREAL
 ... * * * * *
 * * * * *
 DMC546 412" LAQSQMLRTKAMREKEEQRLRMRYALVRVKFPNGLFIQGTFFNVYEKISDVFFVQSCIL
 * * * * *
 * * * * *
 HP10580 371' QSDWLPFELLASGGQKLSEDE-NLALNECGLVPSALLTFSWDMAVLEDIKAAGAEPSIL
 ... * * * * *
 * * * * *
 DMC546 472" ADESILDFSLVSNSDGKLGEDELEKTLVDCKLIPTLILLFSANDTPAPLQTDINYLKEDLL
 * * * * *
 * * * * *
 HP10580 430' KPELLSAIEKLL
 DMC546 532" MLVQAM